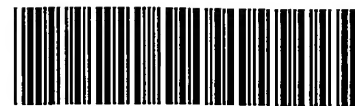# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/542,682 _____

Source: _____ PCT _____

Date Processed by STIC: _____ 07/28/2005 _____

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 07/28/2005
PATENT APPLICATION: US/10/542,682   TIME: 15:36:02

Input Set : **A:\14875-147US1.txt**
Output Set: **N:\CRF4\07282005\J542682.raw**

```
      3 <110> APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
      5 <120> TITLE OF INVENTION: Anti-PCI neutralizing antibodies
      7 <130> FILE REFERENCE: 14875-147US1
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/542,682
C-->  9 <141> CURRENT FILING DATE: 2005-07-19
      9 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/000429
     10 <151> PRIOR FILING DATE: 2004-01-20
     12 <150> PRIOR APPLICATION NUMBER: JP 2003-011529
     13 <151> PRIOR FILING DATE: 2003-01-20
     15 <160> NUMBER OF SEQ ID NOS: 60
     17 <170> SOFTWARE: PatentIn version 3.1
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 27
     21 <212> TYPE: DNA
     22 <213> ORGANISM: Artificial Sequence
     24 <220> FEATURE:
     25 <223> OTHER INFORMATION: Artificially synthesized sequence
     27 <400> SEQUENCE: 1
     28 acgaattcca ccatgcagct cttcctc                          27
     30 <210> SEQ ID NO: 2
     31 <211> LENGTH: 28
     32 <212> TYPE: DNA
     33 <213> ORGANISM: Artificial Sequence
     35 <220> FEATURE:
     36 <223> OTHER INFORMATION: Artificially synthesized sequence
     38 <400> SEQUENCE: 2
     39 ctggatcctc aggggcggtt cactttgc                         28
     41 <210> SEQ ID NO: 3
     42 <211> LENGTH: 26
     43 <212> TYPE: DNA
     44 <213> ORGANISM: Artificial Sequence
     46 <220> FEATURE:
     47 <223> OTHER INFORMATION: Artificially synthesized sequence
     49 <400> SEQUENCE: 3
     50 ttggatccgg ggttcacttt gccaag                           26
     52 <210> SEQ ID NO: 4
     53 <211> LENGTH: 1237
     54 <212> TYPE: DNA
     55 <213> ORGANISM: Artificial
     57 <220> FEATURE:
     58 <223> OTHER INFORMATION: Artificially synthesized sequence encoding human PCI
     60 <220> FEATURE:
     61 <221> NAME/KEY: CDS
```

```
62  <222> LOCATION: (11)..(1228)
64  <400> SEQUENCE: 4
65  gaattccacc atg cag ctc ttc ctc ctc ttg tgc ctg gtg ctt ctc agc      49
66            Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser
67             1                   5                  10
69  cct cag ggg gcc tcc ctt cac cgc cac cac ccc cgg gag atg aag aag      97
70  Pro Gln Gly Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys
71       15                  20                  25
73  aga gtc gag gac ctc cat gta ggt gcc acg gtg gcc ccc agc agc aga     145
74  Arg Val Glu Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg
75   30                  35                  40                  45
77  agg gac ttt acc ttc gac ctc tac agg gtc ttg gct tcc gct gcc ccc     193
78  Arg Asp Phe Thr Phe Asp Leu Tyr Arg Val Leu Ala Ser Ala Ala Pro
79              50                  55                  60
81  agc cag aat atc ttc ttc tcc cct gtg agc atc tcc atg agc ctg gcc     241
82  Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala
83              65                  70                  75
85  atg ctc tcc ctg ggg gct ggg tcc agc aca aag atg cag atc ctg gag     289
86  Met Leu Ser Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu
87              80                  85                  90
89  ggc ctg ggc ctc aac ctc cag aaa agc tca gag gag gag ctg cac aga     337
90  Gly Leu Gly Leu Asn Leu Gln Lys Ser Ser Glu Glu Glu Leu His Arg
91       95                  100                 105
93  ggc ttt cag cag ctc ctt cag gaa ctc aac cag ccc aga gat ggc ttc     385
94  Gly Phe Gln Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe
95  110                 115                 120                 125
97  cag ctg agc ctc ggc aat gcc ctt ttc acc gac ctg gtg gta gac ctg     433
98  Gln Leu Ser Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu
99              130                 135                 140
101 cag gac acc ttc gta agt gcc atg aag acg ctg tac ctg gca gac act     481
102 Gln Asp Thr Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr
103             145                 150                 155
105 ttc ccc acc aac ttt agg gac tct gca ggg gcc atg aag cag atc aat     529
106 Phe Pro Thr Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn
107             160                 165                 170
109 gat tat gtg gca aag caa acg aag ggc aag att gtg gac ttg ctt aag     577
110 Asp Tyr Val Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys
111     175                 180                 185
113 aac ctc gat agc aat gcg gtc gtg atc atg gtg aat tac atc ttc ttt     625
114 Asn Leu Asp Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe
115 190                 195                 200                 205
117 aaa gct aag tgg gag aca agc ttc aac cac aaa ggc acc caa gag caa     673
118 Lys Ala Lys Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln
119             210                 215                 220
121 gac ttc tac gtg acc tcg gag act gtg gtg cgg gta ccc atg atg agc     721
122 Asp Phe Tyr Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser
123             225                 230                 235
125 cgc gag gat cag tat cac tac ctc ctg gac cgg aac ctc tcc tgc agg     769
126 Arg Glu Asp Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg
```

RAW SEQUENCE LISTING   DATE: 07/28/2005
PATENT APPLICATION: US/10/542,682   TIME: 15:36:02

Input Set : A:\14875-147US1.txt
Output Set: N:\CRF4\07282005\J542682.raw

```
127          240                  245                  250
129 gtg gtg ggg gtc ccc tac caa ggc aat gcc acg gct ttg ttc att ctc   817
130 Val Val Gly Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu
131      255                  260                  265
133 ccc agt gag gga aag atg cag cag gtg gag aat gga ctg agt gag aaa   865
134 Pro Ser Glu Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys
135 270                  275                  280                  285
137 acg ctg agg aag tgg ctt aag atg ttc aaa aag agg cag ctc gag ctt   913
138 Thr Leu Arg Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu
139                  290                  295                  300
141 tac ctt ccc aaa ttc tcc att gag ggc tcc tat cag ctg gag aaa gtc   961
142 Tyr Leu Pro Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val
143          305                  310                  315
145 ctc ccc agt ctg ggg atc agt aac gtc ttc acc tcc cat gct gat ctg   1009
146 Leu Pro Ser Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu
147          320                  325                  330
149 tcc ggc atc agc aac cac tca aat atc cag gtg tct gag atg gtg cac   1057
150 Ser Gly Ile Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His
151      335                  340                  345
153 aaa gct gtg gtg gag gtg gac gag tcg gga acc aga gca gcg gca gcc   1105
154 Lys Ala Val Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala
155 350                  355                  360                  365
157 acg ggg aca ata ttc act ttc agg tcg gcc cgc ctg aac tct cag agg   1153
158 Thr Gly Thr Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg
159                  370                  375                  380
161 cta gtg ttc aac agg ccc ttt ctg atg ttc att gtg gat aac aac atc   1201
162 Leu Val Phe Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile
163                  385                  390                  395
165 ctc ttc ctt ggc aaa gtg aac cgc ccc tgaggatcc                     1237
166 Leu Phe Leu Gly Lys Val Asn Arg Pro
167          400                  405
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 406
172 <212> TYPE: PRT
173 <213> ORGANISM: Artificial
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Human PCI
178 <220> FEATURE:
179 <221> NAME/KEY: sig_peptide
180 <222> LOCATION: (1)..(19)
182 <400> SEQUENCE: 5
183 Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser Pro Gln Gly
184 1                   5                  10                  15
186 Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys Arg Val Glu
187              20                  25                  30
189 Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe
190          35                  40                  45
192 Thr Phe Asp Leu Tyr Arg Val Leu Ala Ser Ala Ala Pro Ser Gln Asn
193      50                  55                  60
```

```
195 Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser
196  65              70              75                      80
198 Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly
199              85              90                      95
201 Leu Asn Leu Gln Lys Ser Ser Glu Glu Glu Leu His Arg Gly Phe Gln
202          100             105             110
204 Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe Gln Leu Ser
205          115             120             125
207 Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu Gln Asp Thr
208      130             135             140
210 Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr
211 145             150             155                     160
213 Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn Asp Tyr Val
214              165             170             175
216 Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp
217          180             185             190
219 Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys
220          195             200             205
222 Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr
223      210             215             220
225 Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp
226 225             230             235                     240
228 Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly
229              245             250                     255
231 Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu
232          260             265             270
234 Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg
235          275             280             285
237 Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro
238      290             295             300
240 Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val Leu Pro Ser
241 305             310             315                     320
243 Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu Ser Gly Ile
244              325             330             335
246 Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val
247              340             345             350
249 Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr
250          355             360             365
252 Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe
253      370             375             380
255 Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile Leu Phe Leu
256 385             390             395                     400
258 Gly Lys Val Asn Arg Pro
259              405
262 <210> SEQ ID NO: 6
263 <211> LENGTH: 1261
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial
267 <220> FEATURE:
```

RAW SEQUENCE LISTING   DATE: 07/28/2005
PATENT APPLICATION: US/10/542,682   TIME: 15:36:02

Input Set : A:\14875-147US1.txt
Output Set: N:\CRF4\07282005\J542682.raw

```
 268 <223> OTHER INFORMATION: Artificially synthesized DNA encoding human PCI with Flag-
tag
 270 <220> FEATURE:
 271 <221> NAME/KEY: CDS
 272 <222> LOCATION: (11)..(1258)
 274 <400> SEQUENCE: 6
 275 gaattccacc atg cag ctc ttc ctc ctc ttg tgc ctg gtg ctt ctc agc      49
 276            Met Gln Leu Phe Leu Leu Leu Cys Leu Val Leu Leu Ser
 277             1               5                  10
 279 cct cag ggg gcc tcc ctt cac cgc cac cac ccc cgg gag atg aag aag      97
 280 Pro Gln Gly Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys
 281     15                  20                  25
 283 aga gtc gag gac ctc cat gta ggt gcc acg gtg gcc ccc agc agc aga     145
 284 Arg Val Glu Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg
 285 30                  35                  40                  45
 287 agg gac ttt acc ttc gac ctc tac agg gtc ttg gct tcc gct gcc ccc     193
 288 Arg Asp Phe Thr Phe Asp Leu Tyr Arg Val Leu Ala Ser Ala Ala Pro
 289                 50                  55                  60
 291 agc cag aat atc ttc ttc tcc cct gtg agc atc tcc atg agc ctg gcc     241
 292 Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala
 293                 65                  70                  75
 295 atg ctc tcc ctg ggg gct ggg tcc agc aca aag atg cag atc ctg gag     289
 296 Met Leu Ser Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu
 297             80                  85                  90
 299 ggc ctg ggc ctc aac ctc cag aaa agc tca gag gag gag ctg cac aga     337
 300 Gly Leu Gly Leu Asn Leu Gln Lys Ser Ser Glu Glu Glu Leu His Arg
 301     95                  100                 105
 303 ggc ttt cag cag ctc ctt cag gaa ctc aac cag ccc aga gat ggc ttc     385
 304 Gly Phe Gln Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe
 305 110                 115                 120                 125
 307 cag ctg agc ctc ggc aat gcc ctt ttc acc gac ctg gtg gta gac ctg     433
 308 Gln Leu Ser Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu
 309                 130                 135                 140
 311 cag gac acc ttc gta agt gcc atg aag acg ctg tac ctg gca gac act     481
 312 Gln Asp Thr Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr
 313                 145                 150                 155
 315 ttc ccc acc aac ttt agg gac tct gca ggg gcc atg aag cag atc aat     529
 316 Phe Pro Thr Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn
 317             160                 165                 170
 319 gat tat gtg gca aag caa acg aag ggc aag att gtg gac ttg ctt aag     577
 320 Asp Tyr Val Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys
 321     175                 180                 185
 323 aac ctc gat agc aat gcg gtc gtg atc atg gtg aat tac atc ttc ttt     625
 324 Asn Leu Asp Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe
 325 190                 195                 200                 205
 327 aaa gct aag tgg gag aca agc ttc aac cac aaa ggc acc caa gag caa     673
 328 Lys Ala Lys Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln
 329             210                 215                 220
 331 gac ttc tac gtg acc tcg gag act gtg gtg cgg gta ccc atg atg agc     721
 332 Asp Phe Tyr Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/28/2005
PATENT APPLICATION: US/10/542,682   TIME: 15:36:03

Input Set : A:\14875-147US1.txt
Output Set: N:\CRF4\07282005\J542682.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:49; Xaa Pos. 2,3,4
Seq#:50; Xaa Pos. 4,5,6,7,9,10,14,17
Seq#:51; Xaa Pos. 6,7
Seq#:53; Xaa Pos. 10,13
Seq#:54; Xaa Pos. 1
Seq#:55; Xaa Pos. 3,6,7
Seq#:58; Xaa Pos. 8
Seq#:59; Xaa Pos. 2

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,57

VERIFICATION SUMMARY　　　　　　　　　　DATE: 07/28/2005
PATENT APPLICATION:　**US/10/542,682**　　　TIME: 15:36:03

Input Set :　**A:\14875-147US1.txt**
Output Set: **N:\CRF4\07282005\J542682.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
M:341 Repeated in SeqNo=50
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:1316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:1337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:1365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
```